# WEST Search History

DATE: Thursday, May 01, 2003

| Set Name side by side | Query | Hit Count | Set Name result set |
|---|---|---|---|
| *DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR* | | | |
| L18 | (random adj2 peptide adj2 library) and target adj5 (fungus or plant adj pathogen) | 3 | L18 |
| *DB=USPT; PLUR=YES; OP=OR* | | | |
| L17 | 6197517.pn. | 1 | L17 |
| *DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR* | | | |
| L16 | L14 and target adj4 fungus | 3 | L16 |
| L15 | L14 and fungus | 652 | L15 |
| L14 | L13 and screen | 1511 | L14 |
| L13 | random adj2 peptide adj2 library | 1715 | L13 |
| L12 | L11 and (fungus adj5 plants) | 9 | L12 |
| L11 | random adj5 library adj5 (oligonucleotide or oligo or nucleotide) | 134 | L11 |
| L10 | L6 and (plant adj4 fungus) | 0 | L10 |
| *DB=USPT; PLUR=YES; OP=OR* | | | |
| L9 | L6 and plant adj4 fungus | 0 | L9 |
| L8 | L6 and (fungi or plant or capsici) | 37 | L8 |
| L7 | L6 and fungi or plant or capsici | 202726 | L7 |
| L6 | random adj5 library adj5 (oligonucleotide or oligo or nucleotide) | 87 | L6 |
| L5 | random adj5 library adj5 (oligo or oligonucleotides or nucleotides) adj5 (fungi or plant) | 0 | L5 |
| L4 | L3 and non adj (immunoglobulin or Ig) | 51 | L4 |
| L3 | L2 and random adj4 library | 1115 | L3 |
| L2 | L1 and fung$ | 15610 | L2 |
| L1 | peptides | 63292 | L1 |

END OF SEARCH HISTORY

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=> file ca medlin
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

FILE 'CA' ENTERED AT 14:07:12 ON 01 MAY 2003
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FILE 'MEDLINE' ENTERED AT 14:07:12 ON 01 MAY 2003

=> s random(5w)peptide(5w)libraries
L1          393 RANDOM(5W) PEPTIDE(5W) LIBRARIES

=> s l1 and target(5w)fung?
L2            0 L1 AND TARGET(5W) FUNG?

=> s l1 and phage
L3          270 L1 AND PHAGE

=> s l3 and fung?(5w)target
L4            0 L3 AND FUNG?(5W) TARGET

=> s l3 and plant(5w)fung?
L5            0 L3 AND PLANT(5W) FUNG?

=> s l1 and plant(2w)disease
L6            0 L1 AND PLANT(2W) DISEASE

=> s l3 and random(2w)(oligo or oligonucleotide)
L7            2 L3 AND RANDOM(2W)(OLIGO OR OLIGONUCLEOTIDE)

=> d l7 1-2 ti au so py ab

L7   ANSWER 1 OF 2  CA  COPYRIGHT 2003 ACS
TI   Isolation of peptides that mimic epitopes on a malarial antigen from
     random peptide libraries displayed on
     phage
AU   Adda, Christopher G.; Tilley, Leann; Anders, Robin F.; Foley, Michael
SO   Infection and Immunity (1999), 67(9), 4679-4688
     CODEN: INFIBR; ISSN: 0019-9567
PY   1999
AB   The ring-infected erythrocyte surface antigen (RESA) is a dense-granule
     protein of Plasmodium falciparum which binds to the cytoskeletal structure
     of the erythrocyte after parasite invasion.  It is currently under trial
     as a vaccine candidate.  In an effort to characterize further the antibody
     responses to this antigen, the authors have panned two independent
     libraries of random peptides expressed on the surface of filamentous
     phage with a monoclonal antibody (MAb 18/2) against RESA.  One
     library consisted of a potentially constrained 17-mer peptide fused with
     the gpVIII phage coat protein, and the other displayed an
     unconstrained 15-mer as a fusion with the minor phage coat
     protein gpIII.  Several rounds of biopanning resulted in enrichment from
     both libraries clones that interacted specifically with MAb 18/2 in
     protein-blotting and ELISA expts.  Nucleotide sequencing of the
     random oligonucleotide insert revealed a common
     predominant motif: (S/T)AVDD.  Several other clones had related but
     degenerate motifs.  Thus, a monoclonal antibody against a malarial antigen
     can select common mimotopes from different random
     peptide libraries.  The authors envisage many uses for
     this technol. in malaria research.
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L7 ANSWER 2 OF 2 MEDLINE
TI Isolation of peptides that mimic epitopes on a malarial antigen from **random peptide libraries** displayed on **phage**.
AU Adda C G; Tilley L; Anders R F; Foley M
SO INFECTION AND IMMUNITY, (1999 Sep) 67 (9) 4679-88.
Journal code: 0246127. ISSN: 0019-9567.
PY 1999
AB The ring-infected erythrocyte surface antigen (RESA) is a dense-granule protein of Plasmodium falciparum which binds to the cytoskeletal structure of the erythrocyte after parasite invasion. It is currently under trial as a vaccine candidate. In an effort to characterize further the antibody responses to this antigen, we have panned two independent libraries of random peptides expressed on the surface of filamentous **phage** with a monoclonal antibody (MAb 18/2) against RESA. One library consisted of a potentially constrained 17-mer peptide fused with the gpVIII **phage** coat protein, and the other displayed an unconstrained 15-mer as a fusion with the minor **phage** coat protein gpIII. Several rounds of biopanning resulted in enrichment from both libraries clones that interacted specifically with MAb 18/2 in protein-blotting and enzyme-linked immunosorbent assay experiments. Nucleotide sequencing of the **random oligonucleotide** insert revealed a common predominant motif: (S/T)AVDD. Several other clones had related but degenerate motifs. Thus, a monoclonal antibody against a malarial antigen can select common mimotopes from different **random peptide libraries**. We envisage many uses for this technology in malaria research.

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(FILE 'HOME' ENTERED AT 14:07:00 ON 01 MAY 2003)

FILE 'CA, MEDLINE' ENTERED AT 14:07:12 ON 01 MAY 2003
L1 393 S RANDOM(5W)PEPTIDE(5W)LIBRARIES
L2 0 S L1 AND TARGET(5W)FUNG?
L3 270 S L1 AND PHAGE
L4 0 S L3 AND FUNG?(5W)TARGET
L5 0 S L3 AND PLANT(5W)FUNG?
L6 0 S L1 AND PLANT(2W)DISEASE
L7 2 S L3 AND RANDOM(2W)(OLIGO OR OLIGONUCLEOTIDE)

=> s fung?
L8 289743 FUNG?

=> s l8 and target
L9 4610 L8 AND TARGET

=> s l9 and (peptide or oligonucleotide)(5w)libr?
L10 22 L9 AND (PEPTIDE OR OLIGONUCLEOTIDE)(5W) LIBR?

=> d l10 1-22 ti au so py ab

L10 ANSWER 1 OF 22 CA COPYRIGHT 2003 ACS
TI Methods for the identification of peptidyl compounds interacting with extracellular **target** molecules
IN Hagen, Frederick S.; Woodbury, Richard G.; Oort, Pieter J.
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
PY 2003
AB The present invention provides libraries expressing **peptide libraries** on the extracellular cell surface of host cells and methods for identifying peptides that bind extracellular **target** mols. under the physiol. conditions encountered in biol. fluids and

secretions. The present invention is also directed to vectors for expressing gene fusion proteins and for targeting those fusion proteins to the extracellular cell surface.

L10 ANSWER 2 OF 22 CA COPYRIGHT 2003 ACS
TI Methods of using randomized libraries of zinc finger proteins for the identification of gene function
IN Case, Casey C.; Liu, Qiang; Rebar, Edward J.; Wolffe, Alan P.
SO U.S. Pat. Appl. Publ., 26 pp., Cont.-in-part of U.S. Ser. No. 456,100, abandoned.
CODEN: USXXCO
PY 2002
2003
AB The present invention relates to methods of using libraries of randomized zinc finger proteins to identify genes assocd. with selected phenotypes. The present invention relates to methods of using libraries of randomized zinc finger proteins to identify genes assocd. with selected phenotypes. Zinc finger proteins are DNA binding proteins typically involved in transcription regulation. The randomized zinc finger protein library was generated by three methods called finger grafting, DNA shuffling or codon doping and the transfection vectors contain individual recombinant zinc finger protein gene were transformed into **target** cells. The **target** cells showing selected phenotypes were isolated to analyze the genes with expression regulated by the introduction of randomized zinc finger protein. This invention provides a novel method to discover genes and regulatory elements which expressions are regulated by zinc finger proteins.

L10 ANSWER 3 OF 22 CA COPYRIGHT 2003 ACS
TI Drug design against drug resistant mutants using directed evolution and **target** protein conformation changes
IN Stevens, Raymond C.; Orencia, Maria C.; Yoon, Jun S.; Hanson, Michael A.
SO PCT Int. Appl., 82 pp.
CODEN: PIXXD2
PY 2002
2002
AB The present invention provides methods for identifying new drugs and potential inhibitors and modulators of drug-resistant variants of a **target** protein of a drug of interest. A drug-resistant variant according to the invention has at least one mutation resulting in a structural change, an activity change or a stability change as compared to the **target** protein. Such variants would include natural variants such as those encountered in the clinic, but preferably variants are selected by directed evolution methodol. The present invention relates to methods for designing new drugs useful against drug-resistant bacterial cells, viruses, mammalian cells and the like. The method involves identifying a **target** protein of the drug, selecting for drug-resistant variants that have an altered **target** protein (variant protein) by directed evolution, detg. the three dimensional structure of the **target** and variant proteins and designing a new drug that can be effective against at least one drug-resistant variant. The present invention can be used to predict future mutations that lead to drug resistance and the type of drugs that are effective to combat such resistance.

L10 ANSWER 4 OF 22 CA COPYRIGHT 2003 ACS
TI Biopanning and rapid analysis of selective interactive ligands (BRASIL)
IN Arap, Wadih; Pasqualini, Renata
SO PCT Int. Appl., 167 pp.
CODEN: PIXXD2
PY 2002
2002
2002
AB The present invention concerns novel methods of identifying peptide

sequences that selectively bind to targets. In alternative embodiments, targets may comprise cells or clumps of cells, particles attached to chems. compds., mols. or aggregates, or parasites. In preferred embodiments, **target** cells are sorted before exposure to the phage library. The general method, Biopanning and Rapid Anal. of Selective Interactive Ligands (BRASIL) provides for rapid and efficient sepn. of phage that bind to targets, while preserving unbound phage. BRASIL may be used in preselection procedure to subtract phage that bind non-specifically to a first **target** before exposing the subtracted library to a second **target**. Certain embodiments concern targeting peptides identified by BRASIL and methods of use of such peptides for targeted delivery of therapeutic agents or imaging agents or diagnosis or treatment of diseases. Novel compns. comprising a first phase, second phase, **target** and a phage library are also disclosed. BASIL is exemplified by screening for targeting peptides for (1) VEGF in HUVEC cells, (2) the Molt-4 leukemia cell line, (3) urothelial tissue (human bladder wall), (4) mesenchymal stem cells, and (5) screening for bone marrow targeting peptides.

L10 ANSWER 5 OF 22 CA COPYRIGHT 2003 ACS
TI Selection of peptides with antibody-like properties
IN Kodadek, Thomas J.
SO U.S. Pat. Appl. Publ., 33 pp.
CODEN: USXXCO
PY 2001
AB The present invention provides a highly sensitive screening assay for the identification of peptide binding partners to virtually any peptide or polypeptide ligand. Utilizing an expression-repression readout system, the inventors have screened libraries of peptides and identified relatively small peptide mols. that bind to the provided **target**. Fusion proteins contg. GST linked to GFP (GG) or to MBP (GM) were prepd. having interleukin converting enzyme-cleavable linkers. The linker in GG was derived from the pro-IL-1.beta.-derived epitope against which a peptide called LEPB was isolated. Only the substrate contg. the epitope recognized by LEPB was protected from cleavage.

L10 ANSWER 6 OF 22 CA COPYRIGHT 2003 ACS
TI Methods for modulating cellular and organismal phenotypes by identification of recombinant regulatory polynucleotides
IN Stemmer, Willem P. C.; Minshull, Jeremy; Keenan, Robert J.
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
PY 2001
2002
2001
2003
AB Methods for identifying and controlling the genetic and metabolic pathways underlying complex phenotypes are provided. Conjoint polynucleotide segments that contribute to or disrupt elements of a multigenic phenotype are produced and expressed in cells of interest. Conjoint polynucleotide segments are recombined and/or mutated to give rise to libraries of recombinant concatemers which are expressed in cells of interest. Libraries of conjoint polynucleotide segments and recombinant concatemers are expressed episomally or integrated into the DNA of organelles or chromosomes. Cells are screened or selected to identify members of the population of cells exhibiting a desired phenotype. Libraries and vectors comprising conjoint polynucleotide segments and recombinant concatemers, as well as cells expressing such libraries and vectors or their components are provided. Possible applications of the invention include manipulation of soybean seed oil biosynthesis, identification of cellular factors inducing or affecting differentiation, and identification and optimization of peptide modulators of cellular targets (e.g. enzymes).

L10 ANSWER 7 OF 22 CA COPYRIGHT 2003 ACS

TI Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs
IN Roberts, Christopher J.
SO U.S., 91 pp.
CODEN: USXXAM
PY 2001
AB The present invention relates to genes in Saccharomyces cerevisiae which are essential for germination and proliferation of S. cerevisiae and using the identified genes or their encoded proteins as targets for highly specific antifungal agents, insecticides, herbicides and anti-proliferation drugs. Specifically, the present invention relates to essential genes YDR141C, YDR091C, YOL022C, YOL026C, YOL034W, and YOL077C. The present invention provides antisense mols. and ribozymes comprising sequences complementary to the sequences of mRNAs of essential genes that function to inhibit the essential genes. The antisense oligonucleotides and ribozymes can be used to prevent **fungal** contamination in cell culture. The present invention also provides neutralizing antibodies to proteins encoded by essential genes that bind to and inactivate the essential gene products. The present invention further provides pharmaceutical compns. for treating **fungal** and proliferative diseases, as well as methods of treatment of **fungal** and proliferative diseases.

L10 ANSWER 8 OF 22 CA COPYRIGHT 2003 ACS
TI Targeted cloning of genes and gene clusters using gene-specific degenerate primers
IN Fomenkov, Alexey; Huang, Yiping; Chaparian, Michael G.; Zheng, Shu-Xian
SO PCT Int. Appl., 74 pp.
CODEN: PIXXD2
PY 2001
2002
AB There is provided a method of targeted cloning of genes and gene clusters by directly isolating the DNA of interest from a mixed population, thereby permitting the construction of a very targeted, highly enriched library. Also provided are several unique methods for cloning the genes provided by this method and the probes used in connection with this method. This is accomplished by directly cloning the **target** gene from the source DNA using one of several novel methods presented, for example by creating template derived primers contg. **target** oligonucleotides, adding these template derived primers to a sample of DNA and performing PCR to replicate those genes targeted by the template derived primers. As an example, octamer and decamer **oligonucleotide libraries** were generated by performing a k-tuple search and anal. using a proprietary gene database. This database consisted of 15 genera representing 34 bacterial and 4 **fungal** species, and 38 protein coding genes. The species included in this database were represented in a weighted fashion based on the known/perceived frequency and importance of secondary metabolite prodn. Of the nearly 65,000 octamers calcd., only a subset of approx. 200, or approx. 0.3 %, were frequently present within every or most of the genes included in the database, and thus useful for universal PCR cloning. An example of 25 octamers and 12 decamers generated and used successfully for cloning are shown. The methods provide the degenerate cloning of the entire family of related **target** genes from a mixed DNA sample. This collection of related genes is then used to affinity purify and clone larger **target** gene contg. fragments from the sample, representing assocd. biosynthetic pathway genes. Also provided are the genes assocd. biosynthetic pathway and the probes used in connection with this method. The invention is exemplified by cloning gene cluster involved in aminoglycoside and .beta.-lactam pathway from S. griseus genomic libraries using primers targeted to related genes (including dhfr2, acvs, ipns, strB1, strD, and stsC), and recA to capture DNA fragments from Streptomyces griseus chromosomal DNA.

L10 ANSWER 9 OF 22 CA COPYRIGHT 2003 ACS
TI Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs
IN Roberts, Christopher J.
SO PCT Int. Appl., 127 pp.
CODEN: PIXXD2
PY 2000
2001
2001
AB The present invention relates to genes in Saccharomyces cerevisiae which are essential for germination and proliferation of S. cerevisiae and using the identified genes or their encoded proteins as targets for highly specific antifungal agents, insecticides, herbicides, and anti-proliferation drugs. The present invention provides antisense mols. and ribozymes comprising sequences complementary to the sequences of mRNAs of essential genes that function to inhibit the essential genes. The present invention also provides neutralizing antibodies to proteins encoded by essential genes that bind to and inactivate the essential gene products. The present invention further provides pharmaceutical compns. for treating **fungal** and proliferative diseases, as well as methods of treatment of **fungal** and proliferative diseases.

L10 ANSWER 10 OF 22 CA COPYRIGHT 2003 ACS
TI Identification of essential genes of yeast as targets for medical and agricultural **fungicides**
IN Dimster-Denk, Dago F.
SO PCT Int. Appl., 156 pp.
CODEN: PIXXD2
PY 2000
2001
2002
AB The present invention relates to methods of identifying genes in Saccharomyces cerevisiae which are essential for germination and proliferation of S. cerevisiae and using the identified genes or their encoded proteins as targets for highly specific antifungal agents, insecticides, herbicides and anti-proliferation drugs. The present invention also provides a method to systematically analyze the S. cerevisiae genome to identify essential genes for use as targets for antifungal agents, insecticides, herbicides and anti-proliferation drugs. The present invention provides antisense mols. and ribozymes comprising sequences complementary to the sequences of mRNAs of essential genes that function to inhibit the essential genes. The present invention also provides neutralizing antibodies to proteins encoded by essential genes that bind to and inactivate the essential gene products. A PCR method for generating knockout mutants that uses sequence information from the yeast genome sequencing project in primer design is described. A set of genes essential for spore germination and outgrowth is identified. These genes show little or no similarity to known gene families.

L10 ANSWER 11 OF 22 CA COPYRIGHT 2003 ACS
TI Recombinant vectors expressing multiple costimulatory molecules, host cell infection, and uses in immunogenic applications
IN Schlom, Jeffrey; Hodge, James; Panicali, Dennis
SO PCT Int. Appl., 188 pp.
CODEN: PIXXD2
PY 2000
2001
2002
AB The present invention provides recombinant vectors encoding and expressing at least three or more costimulatory mols and host cells infected by the vector. The recombinant vector may addnl. contain a gene encoding one or more **target** antigens or immunol. epitope as well as cytokine, chemokine, or Flt-3L. A method of making a recombinant poxvirus, of enhancing an immune response of an individual by administering a

2002
2002
2001
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AB Methods are disclosed for screening compd. libraries using frontal chromatog. in combination with mass spectrometry to identify and rank those members of the library that bind to a **target** receptor. Methods are also disclosed which permit a compd. library to be rapidly screened to det. if any member of the library has an affinity for the **target** receptor as measured by a pre-selected indicator compd.

L10 ANSWER 14 OF 22 CA COPYRIGHT 2003 ACS
TI Frontal chromatog.-mass spectrometry apparatus for screening compound libraries
IN Hindsgaul, Ole; Schriemer, David C.
SO PCT Int. Appl., 80 pp.
CODEN: PIXXD2
PY 1999
2000
1998
2002
2002
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2003

AB Disclosed is an app. for screening compd. libraries using frontal chromatog. in combination with mass spectrometry to identify and rank those members of the library that bind to a **target** receptor. The app. of this invention also permit a compd. library to be rapidly screened to det. if any member of the library has an affinity for the **target** receptor as measured by a pre-selected indicator compd.

L10 ANSWER 15 OF 22 CA COPYRIGHT 2003 ACS
TI Inhibitors of phosphoserine- and phosphothreonine-proline-specific isomerases, and therapeutic use
IN Lu, Kun Ping; Cantley, Lewis C.; Yaffee, Michael; Fischer, Gunter
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
PY 1999
2002
1999
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2002
2000
2001

AB Peptides and peptide mimetics that inhibit phosphoserine- or phosphothreonine-specific peptidyl prolyl isomerases are described. The inhibitor compds. of the invention are useful in the treatment of disorders of cell proliferation, e.g. hyperplastic or neoplastic disorders, wherein treatment of the disorder with the inhibitor results in the arrest of mitosis and apoptosis of the **target** cells.

L10 ANSWER 16 OF 22 CA COPYRIGHT 2003 ACS
TI A method for selecting **target** pathogen-inhibiting substances, and test kits for use therein
IN Lankinen, Hilkka; Heiskanen, Tuomas; Vaheri, Antti; Lundkvist, Ake
SO PCT Int. Appl., 80 pp.

recombinant vector, and of treating or preventing a disease by activating a T lymphocyte, are also presented. Further describes are a method of making a progenitor dendritic cell or dendritic cell, of assessing the efficacy of a vaccine against a **target** antigen, and of screening for novel immunogenic peptides. The synergistic effect of these costimulatory mols. on the enhanced activation of T cells was demonstrated. The degree of T-cell activation using recombinant vectors contg. genes encoding three costimulatory mols. was far greater than the sum of recombinant vector constructs contg. one costimulatory mol. and greater than the use of two costimulatory mols. Results employing the triple costimulatory vectors were most dramatic under conditions of either low levels of first signal or low stimulator to T-cell ratios. This phenomenon was obsd. with both isolated CD4+ and CD8+ T cells. The recombinant vectors of the present invention are useful as immunogenes and vaccines against cancer and pathogenic micro-organisms, and in providing host cells, including dendritic cells and splenocytes with enhanced antigen-presenting functions.

L10 ANSWER 12 OF 22 CA COPYRIGHT 2003 ACS
TI Targeting of specific cell types for removal by the immune system
IN Massey, Robert
SO PCT Int. Appl., 43 pp.
CODEN: PIXXD2
PY 1999
1999
AB This disclosure provides a method of selecting one or more peptides or groups of peptide or protein bound to a carrier (for example, as part of peptide-expressing bacteriophage, from a **peptide** or protein expressing phage **library** or other ligand bound to an immunogenic carrier), that recognize and bind to epitopes exposed on one **target** class of cells or tissue only, and the application of the selected group of peptides or proteins or ligand and their carriers as markers to identify the desired **target** cells or **target** tissue in situ . Desirably, the immune system has been primed to recognize and respond to the carrier of the peptide or protein, so that a **target** cell/carrier/antibody complex is formed. Alternatively, the immune response to the carrier can be generated during treatment. By interposing the carrier between the and the responding antibody, the immune system's tolerance to the **target** is bypassed. Thus, the immune system can be made to **target** any desired cell within the body for elimination by decorating that **target** cell or **target** tissue with a carrier bearing a peptide which specifically binds to the **target** cell. The carrier may be a virus, filamentous bacteriophage, carbohydrate, aggregated protein, prokaryote, eukaryote, yeast, or mammalian cell. The **target** cell or tissue is a tumor, or a cell infected by virus, bacterium, **fungus** or protozoa. The **peptide** or protein expression **library** -contg. compn. may also comprise immunity-stimulating agent or inflammatory response-enhancing agent, such as cytokine, interleukin 2, Flt3 or PI-Ca91.

L10 ANSWER 13 OF 22 CA COPYRIGHT 2003 ACS
TI Methods using frontal chromatography-mass spectrometry for screening compound libraries
IN Hindsgaul, Ole; Schriemer, David C.
SO PCT Int. Appl., 90 pp.
CODEN: PIXXD2
PY 1999
1998
1999
2001
2001
2001
1999

CODEN: PIXXD2
PY 1997
1997
1998
AB A method is disclosed for selecting pathogen-inhibiting substances with high affinity and neutralizing effect by competitive elution using neutralizing substances. The method and system are useful for comparative drug design to provide therapeutically active, protective and/or prophylactic substances and developing combinatorial therapies as well as for pathogen diagnostics. The invention also discloses methods for identifying the mimotype characteristics of the neutralization site of pathogens, esp. enveloped viruses, e.g. hantavirus or respiratory syncytial virus. The invention is further related to ligands obtainable by the method, as well as consensus sequences and parts and repeats of the ligands for use in test kits contg. combinatorial ligand libraries comprising the ligands selected by the method.

L10 ANSWER 17 OF 22 MEDLINE
TI Expression of an antimicrobial peptide via the chloroplast genome to control phytopathogenic bacteria and **fungi**.
AU DeGray G; Rajasekaran K; Smith F; Sanford J; Daniell H
SO PLANT PHYSIOLOGY, (2001 Nov) 127 (3) 852-62.
Journal code: 0401224. ISSN: 0032-0889.
PY 2001
AB The antimicrobial peptide MSI-99, an analog of magainin 2, was expressed via the chloroplast genome to obtain high levels of expression in transgenic tobacco (Nicotiana tabacum var. Petit Havana) plants. Polymerase chain reaction products and Southern blots confirmed integration of MSI-99 into the chloroplast genome and achievement of homoplasmy, whereas northern blots confirmed transcription. Contrary to previous predictions, accumulation of MSI-99 in transgenic chloroplasts did not affect normal growth and development of the transgenic plants. This may be due to differences in the lipid composition of plastid membranes compared with the membranes of susceptible **target** microbes. In vitro assays with protein extracts from T(1) and T(2) plants confirmed that MSI-99 was expressed at high levels to provide 88% (T(1)) and 96% (T(2)) inhibition of growth against Pseudomonas syringae pv tabaci, a major plant pathogen. When germinated in the absence of spectinomycin selection, leaf extracts from T(2) generation plants showed 96% inhibition of growth against P. syringae pv tabaci. In addition, leaf extracts from transgenic plants (T(1)) inhibited the growth of pregerminated spores of three **fungal** species, Aspergillus flavus, Fusarium moniliforme, and Verticillium dahliae, by more than 95% compared with non-transformed control plant extracts. In planta assays with the bacterial pathogen P. syringae pv tabaci resulted in areas of necrosis around the point of inoculation in control leaves, whereas transformed leaves showed no signs of necrosis, demonstrating high-dose release of the peptide at the site of infection by chloroplast lysis. In planta assays with the **fungal** pathogen, Colletotrichum destructivum, showed necrotic anthracnose lesions in non-transformed control leaves, whereas transformed leaves showed no lesions. Genetically engineering crop plants for disease resistance via the chloroplast genome instead of the nuclear genome is desirable to achieve high levels of expression and to prevent pollen-mediated escape of transgenes.

L10 ANSWER 18 OF 22 MEDLINE
TI II. Structure and specificity of the interaction between the FHA2 domain of Rad53 and phosphotyrosyl peptides.
AU Wang P; Byeon I J; Liao H; Beebe K D; Yongkiettrakul S; Pei D; Tsai M D
SO JOURNAL OF MOLECULAR BIOLOGY, (2000 Sep 29) 302 (4) 927-40.
Journal code: 2985088R. ISSN: 0022-2836.
PY 2000
AB The forkhead-associated (FHA) domain is a protein module found in many proteins involved in cell signaling in response to DNA damage. It has

been suggested to bind to pThr sites of its **target** protein. Recently we have determined the first structure of an FHA domain, FHA2 from the yeast protein Rad53, and demonstrated that FHA2 binds to a pTyr-containing peptide (826)EDI(pY)YLD(832) from Rad9, with a moderate affinity (K(d) ca. 100 microM). We now report the solution structure of the complex of FHA2 bound with this pTyr peptide. The structure shows that the phosphate group of pTyr interacts directly with three arginine residues (605, 617, and 620), and that the leucine residue at the +2 position from the pTyr interacts with a hydrophobic surface on FHA2. The sequence specificity of FHA2 was determined by screening a combinatorial pTyr library. The results clearly show that FHA2 recognizes specific sequences C-terminal to pTyr with the following consensus: XX(pY)N(1)N(2)N(3), where N(1)=Leu, Met, Phe, or Ile, N(2)=Tyr, Phe, Leu, or Met, and N(3)=Phe, Leu, or Met. Two of the selected peptides, GF(pY)LYFIR and DV(pY)FYMIR, bind FHA2 with K(d) values of 1.1 and 5.0 microM, respectively. The results, along with other recent reports, demonstrate that the FHA domain is a new class of phosphoprotein-binding domain, capable of binding both pTyr and pThr sequences.


L10 ANSWER 19 OF 22 MEDLINE
TI Combining structure-based design with phage display to create new Cys(2)His(2) zinc finger dimers.
AU Wolfe S A; Ramm E I; Pabo C O
SO STRUCTURE WITH FOLDING & DESIGN, (2000 Jul 15) 8 (7) 739-50.
Journal code: 100889329. ISSN: 0969-2126.
PY 2000
AB BACKGROUND: Several strategies have been reported for the design and selection of novel DNA-binding proteins. Most of these studies have used Cys(2)His(2) zinc finger proteins as a framework, and have focused on constructs that bind DNA in a manner similar to Zif268, with neighboring fingers connected by a canonical (Krüppel-type) linker. This linker does not seem ideal for larger constructs because only modest improvements in affinity are observed when more than three fingers are connected in this manner. Two strategies have been described that allow the productive assembly of more than three canonically linked fingers on a DNA site: connecting sets of fingers using linkers (covalent), or assembling sets of fingers using dimerization domains (non-covalent). RESULTS: Using a combination of structure-based design and phage display, we have developed a new dimerization system for Cys(2)His(2) zinc fingers that allows the assembly of more than three fingers on a desired **target** site. Zinc finger constructs employing this new dimerization system have high affinity and good specificity for their **target** sites both in vitro and in vivo. Constructs that recognize an asymmetric binding site as heterodimers can be obtained through substitutions in the zinc finger and dimerization regions. CONCLUSIONS: Our modular zinc finger dimerization system allows more than three Cys(2)His(2) zinc fingers to be productively assembled on a DNA-binding site. Dimerization may offer certain advantages over covalent linkage for the recognition of large DNA sequences. Our results also illustrate the power of combining structure-based design with phage display in a strategy that assimilates the best features of each method.

L10 ANSWER 20 OF 22 MEDLINE
TI A T-cell epitope determined with random **peptide libraries** and combinatorial peptide chemistry stimulates T cells specific for cutaneous T-cell lymphoma.
AU Linnemann T; Wiesmuller K H; Gellrich S; Kaltoft K; Sterry W; Walden P
SO ANNALS OF ONCOLOGY, (2000) 11 Suppl 1 95-9.
Journal code: 9007735. ISSN: 0923-7534.
PY 2000
AB BACKGROUND: Mycosis **fungoides** is the most frequent T-cell lymphoma of the skin. Despite numerous attempts, no tumour antigens have yet been identified. Only in one case has an idiotype-derived peptide

been found to trigger CTL of the respective patient. The identification of natural antigens requires the cultivation of large amounts of tumour cells in vitro, which has been possible in two exceptional cases. The identification of synthetic epitopes for tumour-specific CTL with random **peptide libraries** can overcome this limitation and is a powerful tool for application in the development of immune therapies for a wide range of patients. MATERIALS AND METHODS: The critical amino acids for the construction of epitopes for the CTCL-specific CTL clone My-La CTL were determined with synthetic **peptide libraries** in positional scanning OX8 format in a standard 61chromium release assay. Sixteen different peptides could be synthesized from the combinatoric of these amino acids with the canonical anchor amino acids for MHC binding. These peptides were tested for their capacity to stimulate My-La CTL and PBMC of an HLA-matched CTCL patient. RESULTS: A synthetic epitope could be identified for My-La CTL, which was recognized in a HLA-restricted manner. The response towards this epitope was comparable to the response towards their natural **target** My-La. Using these synthetic epitopes, T cells of a HLA-matched patient could be induced in vitro and led to the establishment of different cell lines and clones. Some of these lines recognized the peptides as well as the allogenic but HLA-matched tumour cell line My-La, indicating that they are specific for a naturally expressed tumour antigen. CONCLUSIONS: The identification of synthetic epitopes for tumour-specific CTL clones can be used for the development of vaccines for immune therapies of cancer; such peptides can be applied inter-individually. Synthetic epitopes must not correspond to the natural ones, but they can be even more potent as stimulation of specific T cells and can be fine-tuned to increase the success of the therapy.

L10 ANSWER 21 OF 22 MEDLINE
TI Genetic selection of peptide inhibitors of biological pathways.
AU Norman T C; Smith D L; Sorger P K; Drees B L; O'Rourke S M; Hughes T R; Roberts C J; Friend S H; Fields S; Murray A W
SO SCIENCE, (1999 Jul 23) 285 (5427) 591-5.
Journal code: 0404511. ISSN: 0036-8075.
PY 1999
AB Genetic selections were used to find peptides that inhibit biological pathways in budding yeast. The peptides were presented inside cells as peptamers, surface loops on a highly expressed and biologically inert carrier protein, a catalytically inactive derivative of staphylococcal nuclease. Peptamers that inhibited the pheromone signaling pathway, transcriptional silencing, and the spindle checkpoint were isolated. Putative targets for the inhibitors were identified by a combination of two-hybrid analysis and genetic dissection of the **target** pathways. This analysis identified Ydr517w as a component of the spindle checkpoint and reinforced earlier indications that Ste50 has both positive and negative roles in pheromone signaling. Analysis of transcript arrays showed that the peptamers were highly specific in their effects, which suggests that they may be useful reagents in organisms that lack sophisticated genetics as well as for identifying components of existing biological pathways that are potential targets for drug discovery.

L10 ANSWER 22 OF 22 MEDLINE
TI Selection of peptides that functionally replace a zinc finger in the Sp1 transcription factor by using a yeast combinatorial library.
AU Cheng X; Boyer J L; Juliano R L
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1997 Dec 9) 94 (25) 14120-5.
Journal code: 7505876. ISSN: 0027-8424.
PY 1997
AB We have developed a strategy for the identification of peptides able to functionally replace a zinc finger domain in a transcription factor. This strategy could have important ramifications for basic research on gene regulation and for the development of therapeutic agents. In this study

in yeast, we expressed chimeric proteins that included a random **peptide** combinatorial **library** in association with two zinc finger domains and a transactivating domain. The library was screened for chimeric proteins capable of activating transcription from a **target** sequence in the upstream regulatory regions of selectable or reporter genes. In a screen of approximately 1.5 x 10(7) transformants we identified 30 chimeric proteins that exhibited transcriptional activation, some of which were able to discriminate between wild-type and mutant DNA targets. Chimeric library proteins expressed as glutathione S-transferase fusions bound to double-stranded oligonucleotides containing the **target** sequence, suggesting that the chimeras bind directly to DNA. Surprisingly, none of the peptides identified resembled a zinc finger or other well-known transcription factor DNA binding domain.

=> d his

(FILE 'HOME' ENTERED AT 14:07:00 ON 01 MAY 2003)

FILE 'CA, MEDLINE' ENTERED AT 14:07:12 ON 01 MAY 2003

| | | | |
|---|---|---|---|
| L1 | 393 | S | RANDOM(5W)PEPTIDE(5W)LIBRARIES |
| L2 | 0 | S | L1 AND TARGET(5W)FUNG? |
| L3 | 270 | S | L1 AND PHAGE |
| L4 | 0 | S | L3 AND FUNG?(5W)TARGET |
| L5 | 0 | S | L3 AND PLANT(5W)FUNG? |
| L6 | 0 | S | L1 AND PLANT(2W)DISEASE |
| L7 | 2 | S | L3 AND RANDOM(2W)(OLIGO OR OLIGONUCLEOTIDE) |
| L8 | 289743 | S | FUNG? |
| L9 | 4610 | S | L8 AND TARGET |
| L10 | 22 | S | L9 AND (PEPTIDE OR OLIGONUCLEOTIDE)(5W)LIBR? |

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| NEWS 3 | Jun 03 | New e-mail delivery for search results now available |
| NEWS 4 | Aug 08 | PHARMAMarketLetter(PHARMAML) - new on STN |
| NEWS 5 | Aug 19 | Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN |
| NEWS 6 | Aug 26 | Sequence searching in REGISTRY enhanced |
| NEWS 7 | Sep 03 | JAPIO has been reloaded and enhanced |
| NEWS 8 | Sep 16 | Experimental properties added to the REGISTRY file |
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| NEWS 21 | Feb 24 | METADEX enhancements |
| NEWS 22 | Feb 24 | PCTGEN now available on STN |
| NEWS 23 | Feb 24 | TEMA now available on STN |
| NEWS 24 | Feb 26 | NTIS now allows simultaneous left and right truncation |
| NEWS 25 | Feb 26 | PCTFULL now contains images |
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FILE 'HOME' ENTERED AT 13:27:58 ON 01 MAY 2003

=> file reg

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|---|---|---|
| FULL ESTIMATED COST | 0.63 | 0.63 |

FILE 'REGISTRY' ENTERED AT 13:29:43 ON 01 MAY 2003
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http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=> sgcagnn(nnn)?/sqsn
SGCAGNN(NNN)? IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter "HELP COMMANDS" at an arrow prompt (=>).

=> s gcagnn(nnn)?/sqsn
COMMAND INTERRUPTED
If this message appears repeatedly, please notify the Help Desk.
Enter "HELP STN" for information on contacting the nearest STN Help Desk by telephone or via SEND in the STNMAIL file.

=> s gcagnn(nnn)?/sqen
GAPS, WILDCARDS, AND BRACKETS ARE INVALID FOR "EXACT" SEQUENCE FIELD CODES.

=> s gcagnn(nnn)7/sqsn
7 IS NOT A VALID NUCLEIC ACID SYMBOL

=> s gcagnn(nnn)/sqsn
COMMAND INTERRUPTED

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If this message appears repeatedly, please notify the Help Desk.
Enter "HELP STN" for information on contacting the nearest STN Help
Desk by telephone or via SEND in the STNMAIL file.

=> s gcagnn(nnn)/sqen
             0 GCAGNN(NNN)/SQEN
         68523 SQL=9
L1           0 GCAGNN(NNN)/SQEN
                 (GCAGNN(NNN)/SQEN AND SQL=9)

=> slvpmlsfaxxxxxxxxxxxxxxxpaegddpaka/sqep
SLVPMLSFAXXXXXXXXXXXXXXXPAEGDDPAKA IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s lvpmlsfaxxxxxxxxxxxxxxxxpaegddpaka/sqep
             1 LVPMLSFAXXXXXXXXXXXXXXXXPAEGDDPAKA/SQEP
         31633 SQL=33
L2           1 LVPMLSFAXXXXXXXXXXXXXXXXPAEGDDPAKA/SQEP
                 (LVPMLSFAXXXXXXXXXXXXXXXXPAEGDDPAKA/SQEP AND SQL=33)

=> slvpmlsfaxxxxxxxxxxxxxxxxpaegddpaka/sqsp
SLVPMLSFAXXXXXXXXXXXXXXXXPAEGDDPAKA IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s lvpmlsfaxxxxxxxxxxxxxxxxpaegddpaka/sqsp
L3           2 LVPMLSFAXXXXXXXXXXXXXXXXPAEGDDPAKA/SQSP

=> file ca medline biosis
COST IN U.S. DOLLARS                          SINCE FILE      TOTAL
                                                   ENTRY    SESSION
FULL ESTIMATED COST                               43.10      43.73

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FILE 'MEDLINE' ENTERED AT 13:35:42 ON 01 MAY 2003

FILE 'BIOSIS' ENTERED AT 13:35:42 ON 01 MAY 2003
COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC.(R)

=> s l1
L4           0 L1

=> s l2
L5           1 L2

=> s l3
L6           1 L3

=> d l5 ti au so py ab

L5   ANSWER 1 OF 1  CA  COPYRIGHT 2003 ACS
TI   Phage display selection and compositions of peptides inducing premature
     encystment of Phytophthora zoospores
IN   English, James T.; Schmidt, Francis J.; Smith, George P.; Morris, Roy O.;
     Bishop-Hurley, Sharon
SO   PCT Int. Appl., 72 pp.
     CODEN: PIXXD2
PY   2001
```

2003
2002
AB A method for the identification of peptides having an affinity for the surface of fungi is provided as is a method for the identification of peptides capable of affecting the development of a fungus. Also provided are compns. comprising Phytophthora peptides identified using the method of the present invention. In addn., isolated polynucleotides, vectors, expression cassettes and transformed cells capable of expressing peptides identified by the method of the present invention are provided. Phage clones from a f8-1 library which bound to Phytophthora capsici and not P. sojae or P. parasitica zoospores were isolated using a selection and enrichment procedure. The selected phage-displayed peptides induced high or low levels of premature encystment of P. capsici zoospores. The binding affinity and specificity of the phage clones were measured. Synthetic oligonucleotides for an exemplary peptide, clone Pc87, were ligated into an expression vector to produce plasmid pJE-7. Plants transformed with such an expression vector construct may secrete the antifungal peptides, causing nearby zoospores to encyst and thereby disrupting the root-orientation and/or infection process of the pathogen.

=> d l6 au

L6 ANSWER 1 OF 1 CA COPYRIGHT 2003 ACS
IN English, James T.; Schmidt, Francis J.; Smith, George P.; Morris, Roy O.; Bishop-Hurley, Sharon

=> s random(5w)(oligo or oligonucleotide or peptides)
L7 1208 RANDOM(5W)(OLIGO OR OLIGONUCLEOTIDE OR PEPTIDES)

=> s l7 and scre?(5w)(fungi or zoospores or capsici)
L8 0 L7 AND SCRE?(5W)(FUNGI OR ZOOSPORES OR CAPSICI)

=> s l7 and scre?(5w)(fungi or zoospores)
L9 0 L7 AND SCRE?(5W)(FUNGI OR ZOOSPORES)

=> s l7 and (fungi or zoospores)
L10 34 L7 AND (FUNGI OR ZOOSPORES)

=> s l10 and bacteriophage or phage
L11 108612 L10 AND BACTERIOPHAGE OR PHAGE

=> d l10 1-34 ti au so py

L10 ANSWER 1 OF 34 CA COPYRIGHT 2003 ACS
TI Random amplified polymorphic DNA variability among geographic isolates of western gall rust fungus in Canada
AU Li, Changxi; Yeh, Francis C.; Hiratsuka, Yasu
SO Canadian Journal of Forest Research (2001), 31(8), 1304-1311
CODEN: CJFRAR; ISSN: 0045-5067
PY 2001

L10 ANSWER 2 OF 34 CA COPYRIGHT 2003 ACS
TI Novel methods for in vivo identification of enzyme inhibitors from random peptide-chymotrypsin inhibitor 2A (CI-2A) fusion library and their use in drug screening
IN Halkier, Torben; Jespersen, Lene; Jensen, Allan
SO PCT Int. Appl., 136 pp.
CODEN: PIXXD2
PY 2000
2000
2000
2002
2001

2002
2002
2002
2002
2002
2003
2001

L10 ANSWER 3 OF 34 CA COPYRIGHT 2003 ACS
TI Strain typing of ectomycorrhizal basidiomycetes from subalpine Tyrolean forest areas by random amplified polymorphic DNA analysis
AU Haudek, Sandra B.; Gruber, Franz; Kreuzinger, Norbert; Gobl, Friederike; Kubicek, Christian P.
SO Mycorrhiza (1996), 6(1), 35-41
CODEN: MCOREZ; ISSN: 0940-6360
PY 1996

L10 ANSWER 4 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Identification of peptide inhibitors of Pseudomonas aeruginosa exotoxin A function using a yeast two-hybrid approach.
AU Thompson, Crista; Merrill, A. Rod; Mangroo, Dev (1)
SO FEMS Microbiology Letters, (21 January 2003) Vol. 218, No. 1, pp. 85-92. print.
ISSN: 0378-1097.
PY 2003

L10 ANSWER 5 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Emergence of nosocomial candidemia at a teaching hospital in Taiwan from 1981 to 2000: Increased susceptibility of Candida species to fluconazole.
AU Hsueh, Po-Ren (1); Teng, Lee-Jene; Yang, Pan-Chyr; Ho, Shen-Wu; Luh, Kwen-Tay
SO Microbial Drug Resistance, (Winter 2002, 2002) Vol. 8, No. 4, pp. 311-319. print.
ISSN: 1076-6294.
PY 2002

L10 ANSWER 6 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI RAPD markers linked to resistance to downy mildew disease in soybean.
AU Chowdhury, A. K.; Srinives, P. (1); Saksoong, P.; Tongpamnak, P.
SO Euphytica, (2002) Vol. 128, No. 1, pp. 55-60. print.
ISSN: 0014-2336.
PY 2002

L10 ANSWER 7 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Evidence of recombination between net- and spot-type populations of Pyrenophora teres as determined by RAPD analysis.
AU Campbell, Graham F.; Lucas, John A.; Crous, Pedro W. (1)
SO Mycological Research, (May, 2002) Vol. 106, No. 5, pp. 602-608. http://uk.cambridge.org/journals/myc/. print.
ISSN: 0953-7562.
PY 2002

L10 ANSWER 8 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI [Genetic variability in Fusarium oxysporum f.sp. passiflorae. Original Title: Avaliacao da variabilidade genetica em isolados de Fusarium oxysporum f.sp. passiflorae..
AU Miranda, Izabel R. de (1); Oliveira, Neiva T. de (1)
SO Summa Phytopathologica, (Outubro Dezembro, 2001) Vol. 27, No. 4, pp. 375-378. print.
ISSN: 0100-5405.
PY 2001

L10 ANSWER 9 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Random amplified polymorphic DNA variability among geographic isolates of western gall rust fungus in Canada.

AU Li, Changxi; Yeh, Francis C. (1); Hiratsuka, Yasu
SO Canadian Journal of Forest Research, (August, 2001) Vol. 31, No. 8, pp. 1304-1311. print.
ISSN: 0045-5067.
PY 2001

L10 ANSWER 10 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Peptides that mimic Candida albicans-derived beta-1,2-linked mannosides.
AU Jouault, Thierry (1); Fradin, Chantal; Dzierszinski, Florence; Borg-Von-Zepelin, Margareth; Tomavo, Stanislas; Corman, Robert; Trinel, Pierre-Andre; Kerckaert, Jean-Pierre; Poulain, Daniel
SO Glycobiology, (August, 2001) Vol. 11, No. 8, pp. 693-701. print.
ISSN: 0959-6658.
PY 2001

L10 ANSWER 11 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Cloning of random oligonucleotides to create single-insert plasmid libraries.
AU Worthington, Mark T. (1); Pelo, Jared; Luo, Roger Qi
SO Analytical Biochemistry, (July 15, 2001) Vol. 294, No. 2, pp. 169-175. print.
ISSN: 0003-2697.
PY 2001

L10 ANSWER 12 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI The strength of acidic activation domains correlates with their affinity for both transcriptional and non-transcriptional proteins.
AU Melcher, Karsten (1)
SO Journal of Molecular Biology, (1 September, 2000) Vol. 301, No. 5, pp. 1097-1112. print.
ISSN: 0022-2836.
PY 2000

L10 ANSWER 13 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Identification of mimotope peptides which bind to the mycotoxin deoxynivalenol-specific monoclonal antibody.
AU Yuan, Qiaoping; Pestka, James J.; Hespenheide, Brandon M.; Kuhn, Leslie A.; Linz, John E.; Hart, L. Patrick (1)
SO Applied and Environmental Microbiology, (Aug., 1999) Vol. 65, No. 8, pp. 3279-3286.
ISSN: 0099-2240.
PY 1999

L10 ANSWER 14 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Identification of surrogate agonists for the human FPRL-1 receptor by autocrine selection in yeast.
AU Klein, Christine (1); Paul, Jeremy I.; Sauve, Karen; Schmidt, Mary M.; Arcangeli, Loretta; Ransom, John; Trueheart, Joshua; Manfredi, John P.; Broach, James R.; Murphy, Andrew J.
SO Nature Biotechnology, (Dec., 1998) Vol. 16, No. 13, pp. 1334-1337.
ISSN: 1087-0156.
PY 1998

L10 ANSWER 15 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Molecular mapping of the py-1 gene for resistance to corky root rot (Pyrenochaeta lycopersici) in tomato.
AU Dognalar, S.; Dodson, J.; Gabor, B.; Beck-Bunn, T.; Crossman, C.; Tanksley, S. D. (1)
SO Theoretical and Applied Genetics, (Oct., 1998) Vol. 97, No. 5-6, pp. 784-788.
ISSN: 0040-5752.
PY 1998

L10 ANSWER 16 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Transdominant genetic analysis of a growth control pathway.

AU Caponigro, Giordano; Abedi, Majid R.; Hurlburt, Anthony P.; Maxfield, Andrew; Judd, Weston; Kamb, Alexander (1)
SO Proceedings of the National Academy of Sciences of the United States of America, (June 23, 1998) Vol. 95, No. 13, pp. 7508-7513. ISSN: 0027-8424.
PY 1998

L10 ANSWER 17 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Use of random amplified polymorphic DNAs markers to distinguish temperature isolates of Aspergillus fumigatus of Taiwan.
AU Chen, Mao-Yen (1); Chen, Kuei-Yu; Tsay, San-San (1); Chen, Zuei-Ching (1)
SO Taiwania, (Sept., 1997) Vol. 42, No. 3, pp. 201-206. ISSN: 0372-333X.
PY 1997

L10 ANSWER 18 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Xbp1, a stress-induced transcriptional repressor of the Saccharomyces cerevisiae Swi4/Mbp1 family.
AU Mai, Bernard; Breeden, Linda (1)
SO Molecular and Cellular Biology, (1997) Vol. 17, No. 11, pp. 6491-6501. ISSN: 0270-7306.
PY 1997

L10 ANSWER 19 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI RAPD analysis for the characterization of Cercospora sojina isolates.
AU Machado, Marco A. (1); Barros, Everaldo G. De; Vasconcelos, Maria J. V.; Gomes, Jose L. L.; Moreira, Maurilio A.
SO Fitopatologia Brasileira, (1997) Vol. 22, No. 3, pp. 366-369. ISSN: 0100-4158.
PY 1997

L10 ANSWER 20 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Analysis of 21.7 kb DNA sequence from the left arm of chromosome VII reveals 11 open reading frames: Two correspond to new genes.
AU Feuermann, M.; Simeonova, L.; Souciet, J.-L.; Potier, S. (1)
SO Yeast, (1997) Vol. 13, No. 5, pp. 475-477. ISSN: 0749-503X.
PY 1997

L10 ANSWER 21 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Cdc48p interacts with Ufd3p, a WD repeat protein required for ubiquitin-mediated proteolysis in Saccharomyces cerevisiae.
AU Ghislain, Michel; Dohmen, R. Juergen; Levy, Frederic; Varshavsky, Alexander (1)
SO EMBO (European Molecular Biology Organization) Journal, (1996) Vol. 15, No. 18, pp. 4884-4899. ISSN: 0261-4189.
PY 1996

L10 ANSWER 22 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Yeast alpha mating factor structure-activity relationship derived from genetically selected peptide agonists and antagonists of Ste2p.
AU Manfredi, John P. (1); Klein, Christine; Herrero, Juan J.; Byrd, Devon A.; Trueheart, Joshua; Wiesler, William T.; Fowlkes, Dana M.; Broach, James R.
SO Molecular and Cellular Biology, (1996) Vol. 16, No. 9, pp. 4700-4709. ISSN: 0270-7306.
PY 1996

L10 ANSWER 23 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI RAPD analysis of pathogenic variability in Ascochyta rabiei.
AU Fischer, C.; Porta-Puglia, A.; Barz, W.
SO Journal of Phytopathology (Berlin), (1995) Vol. 143, No. 10, pp. 601-607. ISSN: 0931-1785.
PY 1995

L10 ANSWER 24 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Immunodominant epitopes defined by a yeast-expressed library of random fragments of the rabies virus glycoprotein map outside major antigenic sites.
AU Lafay, Florence (1); Benmansour, Abdenour; Chebli, Karim; Flamand, Anne
SO Journal of General Virology, (1996) Vol. 77, No. 2, pp. 339-346.
ISSN: 0022-1317.
PY 1996

L10 ANSWER 25 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Strain typing of ectomycorrhizal basidiomycetes from subalpine Tyrolean forest areas by random amplified polymorphic DNA analysis.
AU Haudek, Sandra B.; Gruber, Franz; Kreuzinger, Norbert; Gobl, Friederike; Kubicek, Christian P.
SO Mycorrhiza, (1996) Vol. 6, No. 1, pp. 35-41.
ISSN: 0940-6360.
PY 1996

L10 ANSWER 26 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI A method of directed random mutagenesis of the yeast chromosome shows that the iso-1-cytochrome c heme ligand His18 is essential.
AU Fumo, Gerard; Spitzer, Jennifer S.; Fetrow, Jacquelyn S. (1)
SO Gene (Amsterdam), (1995) Vol. 164, No. 1, pp. 33-39.
ISSN: 0378-1119.
PY 1995

L10 ANSWER 27 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Sequence of a 9 cntdot 8 kb segment of yeast chromosome II including the three genes of the MAL3 locus and three unidentified open reading frames.
AU Feuermann, M.; Charbonnel, L.; De Montigny, J.; Bloch, J.-C.; Potier, S.; Souciet, J.-L. (1)
SO Yeast, (1995) Vol. 11, No. 7, pp. 667-672.
ISSN: 0749-503X.
PY 1995

L10 ANSWER 28 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Protein-peptide interactions analyzed with the yeast two-hybrid system.
AU Yang, Meijia; Wu, Zining; Fields, Stanley (1)
SO Nucleic Acids Research, (1995) Vol. 23, No. 7, pp. 1152-1156.
ISSN: 0305-1048.
PY 1995

L10 ANSWER 29 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Morphological, pathological, and genetic differentiation of Didymella bryoniae and Phoma ssp. isolated from cucurbits.
AU Keinath, A. P. (1); Farnham, M. W.; Zitter, T. A.
SO Phytopathology, (1995) Vol. 85, No. 3, pp. 364-369.
ISSN: 0031-949X.
PY 1995

L10 ANSWER 30 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Genetic structure of Pyrenophora teres populations determined with random amplified polymorphic DNA markers.
AU Peever, Tobin L. (1); Milgroom, Michael G.
SO Canadian Journal of Botany, (1994) Vol. 72, No. 7, pp. 915-923.
ISSN: 0008-4026.
PY 1994

L10 ANSWER 31 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Novel estrogen response elements identified by genetic selection in yeast are differentially responsive to estrogens and antiestrogens in mammalian cells.
AU Dana, Sharon L. (1); Hoener, Patricia A.; Wheeler, David A.; Lawrence, Charles B.; McDonnell, Donald P.
SO Molecular Endocrinology, (1994) Vol. 8, No. 9, pp. 1193-1207.

ISSN: 0888-8809.
PY 1994

L10 ANSWER 32 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI Molecular Determinants of Bioactivity of the Saccharomyces cerevisiae Lipopeptide Mating Pheromone.
AU Caldwell, Guy A.; Wang, Shu-Hua; Zue, Chu-Biao; Jiang, Ying; Lu, Hui-Fen; Naider, Fred; Becker, Jeffrey M. (1)
SO Journal of Biological Chemistry, (1994) Vol. 269, No. 31, pp. 19817-19826. ISSN: 0021-9258.
PY 1994

L10 ANSWER 33 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI A partial genetic linkage map of slash pine (Pinus elliottii Engelm. var. elliottii) based on random amplified polymorphic DNAs.
AU Nelson, C. D. (1); Nance, W. L.; Doudrick, R. L.
SO Theoretical and Applied Genetics, (1993) Vol. 87, No. 1-2, pp. 145-151. ISSN: 0040-5752.
PY 1993

L10 ANSWER 34 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
TI THE FREE SULFHYDRYL GROUP CYSTEINE 341 OF CARBOXYPEPTIDASE Y FUNCTIONAL EFFECTS OF MUTATIONAL SUBSTITUTIONS.
AU WINTHER J R; BREDDAM K
SO CARLSBERG RES COMMUN, (1987) 52 (4), 263-274. CODEN: CRCODS. ISSN: 0105-1938.
PY 1987

=> d l10 1-34 ab

L10 ANSWER 1 OF 34 CA COPYRIGHT 2003 ACS
AB Geog. variability among western gall rust (WGR) fungus [Endocronartium harknessii (J.P. Moore) Y. Hiratsuka] was studied by random amplified polymorphic DNA (RAPD). Samples were taken from lodgepole pine (Pinus contorta Dougl. ex Loud. var. latifolia Engelm.) host at four locations in British Columbia and Alberta and from jack pine (Pinus banksiana Lamb.) host at nine locations in Alberta, Saskatchewan, Manitoba, and Ontario. Of 90 **random oligonucleotide** primers screened, 9 were chosen for anal. These nine primers consistently amplified 41 sharp and reproducible RAPDs (fragments) of the WGR fungal isolates over several independent runs. Eighteen of the 41 RAPDs were polymorphic (showing the presence of both marker and null phenotypes), of which 15 could discriminate WGR isolates of lodgepole pine hosts from jack pine ones. Of these 15 RAPDs, five were unique to isolates of lodgepole and five to jack pine. The remaining five RAPDs were significantly heterogeneous in the RAPD frequency between WGR isolates of the two host origins. The RAPD pattern of WGR isolates from lodgepole pine was uniform. However, isolates from jack pine differed significantly in the frequency of four RAPDs among locations, with an east-west trend of decreasing similarity in RAPD. Anal. of mol. variance apportioned 76.3, 14.4, and 9.3% of the total RAPD variability to differences among hosts, to differences among locations within hosts, and to differences within locations, resp. The large differentiation between WGR fungal isolates sampled in lodgepole pine and jack pine hosts might suggest that selective pressure for host specificity in sampled populations was strong.

L10 ANSWER 2 OF 34 CA COPYRIGHT 2003 ACS
AB Novel methods (so called CellScreen.RTM. technol.) for in vivo identification enzyme inhibitors from random peptide-chymotrypsin inhibitor 2A (CI-2A) fusion library and their use in drug screening are described. Barley CI-2A from the potato inhibitor I family of protease inhibitors is used as the scaffold to display random peptide sequences in vivo since it can be stably and sufficiently expressed in the nucleus or ER of cultured cells, or displayed on the phage particles and remains

biol. active. Random peptide library is constructed by inserting the random synthetic oligonucleotides or PCR fragments inside the CI-2A loop coding region in the retroviral expression vector and expressed intracellularly. The signal peptide sequence for various intracellular compartments or peptide tag can be fused at the N-terminus of the peptide-CI-2A library for the localization or purifn. purpose. The enzyme inhibitors or their relative RNA can be isolated from the phenotypically altered cells and used for further screening of their interaction partners which has therapeutic potentials.

L10 ANSWER 3 OF 34 CA COPYRIGHT 2003 ACS
AB The application of random amplified polymorphic DNA (RAPD) anal. for the identification of ectomycorrhizal symbionts of spruce (Picea abies) belonging to the genera Boletus, Amanita and Lactarius at and below the species level was investigated. Using both fingerprinting [M13, (GTG)5, (GACA)4] as well as **random oligonucleotide** primers (V1 and V5), a high degree of variability of amplified DNA fragments (band-sharing index 65-80%) was detected between different strains of the same species, hence enabling the identification of individual strains within the same species. The band-sharing index between different species of the same genus (Boletus, Russula and Amanita) was in the range of 20-30%, and similar values were obtained when strains from different taxa were compared. Thus RAPD is too sensitive at this level of relationship and cannot be used to align an unknown symbiont to a given taxon. We therefore conclude that RAPD is a promising tool for the identification of individual strains, and could thus be used to distinguish indigenous and introduced mycorrhizal strains from the same species in natural ecosystems.

L10 ANSWER 4 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The yeast two-hybrid system was used to identify peptide inhibitors of exotoxin A of Pseudomonas aeruginosa with the goal of using these to design peptide-based drugs against the toxin. A **random** peptide library consisting of 107 **peptides** ranging in length from 16 to 63 residues was screened for peptides that interact with the C-domain of exotoxin A. From the 107 transformants screened, three unique peptides of 63, 61 and 25 amino acids in length were found to specifically interact with the enzyme domain. The genes encoding these peptides were cloned and expressed as fusion proteins with the maltose-binding protein. In vitro inhibition measurements indicated that two of the peptides were modest inhibitors of toxin enzyme activity. These peptides now provide the basis for the development of more potent inhibitors, which will serve as lead inhibitors for evolution of potent peptide-based therapeutics.

L10 ANSWER 5 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The incidence of nosocomial Candida fungemia increased 36-fold from 1981 (0.8/10,000 discharges) to 2000 (28.8/10,000 discharges) at the National Taiwan University Hospital, a 2000-bed teaching hospital in northern Taiwan. To understand the current status of resistance to available antifungal agents among Candida species causing invasive infections, the in vitro susceptibilities of 222 isolates (collected from July, 1999-June, 2001) were determined. Among all of the Candida species tested, 6% and 7% were resistant to fluconazole and itraconazole, respectively. The MIC90 values of voriconazole and amphotericin B were 0.5 and 1 mug/ml, respectively, although some isolates of C. krusei (amphotericin B and voriconazole MIC, >64 mug/ml) and C. tropicalis and C. glabrata (voriconazole MICs, >64 mug/ml) were less susceptible to voriconazole or amphotericin B. About one-half of the C. glabrata isolates belonged to susceptible dose-dependent (SDD, 36%) or resistant (12%) categories for fluconazole and 96% belonged to SDD (56%) or resistant (40%) category for itraconazole. When compared with fluconazole susceptibility data of blood Candida isolates recovered from patients treated at the same hospital (NTUH) from two different time periods (January, 1994, to June, 1995, and January, 1997, to June, 1999 described in previous reports), the incidence of increased susceptibility of non-krusei Candida isolates to fluconazole

was evident. This trend of increasing susceptibility for fluconazole did not correlate to the increasing use of this agent in the hospital. None of the random amplified polymorphic DNA patterns generated by arbitrarily primed PCR using four **random oligonucleotide** primers for 14 isolates, which exhibited fluconazole MICs of gtoreq16 mug/ml, were identical, indicating an absence of clonal dissemination among these isolates in the hospital.

L10 ANSWER 6 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB To determine and utilize RAPD markers linked to resistance to downy mildew incited by Peronospora manshurica in soybean, a resistant cultivar 'AGS129' was crossed to a susceptible cultivar 'Nakhon Sawan 1' (NS1). F2 and BC1 populations were advanced from the F1 and evaluated for resistance to the disease. chi2-test demonstrated that the resistance was controlled by a single dominant gene (Rpmx). Near-isogenic lines (NILs) and bulked segregant analysis (BSA) were used to identify RAPD markers linked to the gene. Six DNA bulks namely F5(R), F5(S), BC6F3(R), BC6F3(S), F2(R) and F2(S) were set up by pooling equal amount of DNA from 8 randomly selected plants of each disease response type. A total of 180 **random** sequence decamer **oligonucleotide** primers were used for RAPD analysis. Primer OPH-02 (5' TCGGACGTGA 3') and OPP-10 (5' TCCCGCCTAC 3') generated OPH-021250 and OPP-10831 fragments in donor parent and resistant bulks, but not in the recurrent parent and susceptible ones. Co-segregation analysis using 102 segregating F2 progenies confirmed that both markers were linked to the Rpmx gene controlling downy mildew disease resistance with a genetic distance of 4.9 cm and 23.1 cm, respectively. Marker OPH-021250 was present in 13 of 16 resistant soybean cultivars and absent in susceptible cultivars, thus confirming a potential for MAS outside the mapping population.

L10 ANSWER 7 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The genetic structure of Pyrenophora teres, the causal agent of net blotch of barley, was examined in two fields 30 km apart in the south-western Cape of South Africa. The two fields respectively represented a net- and spot-type population, the two types being distinguished on the basis of symptom expression on differentially susceptible cultivars. The number of isolates sampled from each field was 36 for the net-type population and 29 for the spot-type population. Samples were collected from infected barley leaves from two separate quadrants in each field, the two quadrants positioned in corners of the fields, diagonal to one another. Of the 40 10-mer **random oligonucleotide** primers screened, five produced scorable, reproducible DNA bands suitable for the determination of population structure. A total of 65 loci were produced of which 54 were polymorphic. Genetic analysis of bands produced by one of the primers has revealed single locus segregation in a mating between a net- and spot-type isolate, indicating that RAPD bands can be interpreted as alleles at genetic loci. Total gene diversities determined for all loci resulted in mean indices of 0.063 and 0.082 being obtained respectively for the net- and spot-type populations. Genetic diversity among the two populations was divided into within- (variation between sampling quadrants) and among population components using Nei's GST. A coefficient of genetic differentiation (GS) of 0.0149 was obtained between quadrants within populations while a coefficient (GT) of 0.63 was obtained between the two populations. Genotypic variation revealed 13 distinct multilocus genotypes (haplotypes) in the net-type population while there were 12 in the spot-type population. UPGMA cluster analysis of the two populations together with six progeny from a mating between a net- and spot-type isolate resulted in three main clusters being produced, one for each population and one for the progeny. One isolate collected from the net-type population that did not cluster with the other net-type isolates clustered directly next to the cluster containing the sexual progeny. This isolate also contained a unique spot-type DNA band. This suggested that sexual recombination may be occurring between net- and spot-type isolates under field conditions.

L10 ANSWER 8 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The genetic variability of 15 isolates of Fusarium oxysporum f.sp. passiflorae obtained from different parts of Passiflorae plants, collected in the northeast of Brazil were investigated in terms of DNA polymorphism using RAPD (**Random** Amplified Polymorphic DNA) procedure. Four **oligo** deoxynucleotide primers were selected for the RAPD assays which resulted in 448 bands. The data were analysed into a binary form and a similarity matrix was constructed using JACCARD similarity index. A UPGMA cluster based on JACCARD values was generated using NTSYS (Numerical Taxonomy System, Applied Biostatistics) computer program. A mean coefficient of similarity obtained for pairwise comparisons among isolates was around 62 %. The results presented here showed that the genetic variability among the isolates was very high. No relationship was found between the isolate groupings and their geographic origin or parts of the plants where the isolates was obtained.

L10 ANSWER 9 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Geographic variability among western gall rust (WGR) fungus (Endocronartium harknessii (J.P. Moore) Y. Hiratsuka) was studied by random amplified polymorphic DNA (RAPD). Samples were taken from lodgepole pine (Pinus contorta Dougl. ex Loud. var. latifolia Engelm.) host at four locations in British Columbia and Alberta and from jack pine (Pinus banksiana Lamb.) host at nine locations in Alberta, Saskatchewan, Manitoba, and Ontario. Of 90 **random oligonucleotide** primers screened, 9 were chosen for analysis. These nine primers consistently amplified 41 sharp and reproducible RAPDs (fragments) of the WGR fungal isolates over several independent runs. Eighteen of the 41 RAPDs were polymorphic (showing the presence of both marker and null phenotypes), of which 15 could discriminate WGR isolates of lodgepole pine hosts from jack pine ones. Of these 15 RAPDs, five were unique to isolates of lodgepole and five to jack pine. The remaining five RAPDs were significantly heterogeneous in the RAPD frequency between WGR isolates of the two host origins. The RAPD pattern of WGR isolates from lodgepole pine was uniform. However, isolates from jack pine differed significantly in the frequency of four RAPDs among locations, with an east-west trend of decreasing similarity in RAPD. Analysis of molecular variance apportioned 76.3, 14.4, and 9.3% of the total RAPD variability to differences among hosts, to differences among locations within hosts, and to differences within locations, respectively. The large differentiation between WGR fungal isolates sampled in lodgepole pine and jack pine hosts might suggest that selective pressure for host specificity in sampled populations was strong.

L10 ANSWER 10 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB beta-1,2-linked mannosides from Candida albicans phosphopeptidomannan (PPM) bind to macrophages through a receptor independent from the macrophage alpha-linked mannose receptor and stimulate these cells to secrete immune mediators. Anti-beta-1,2-linked mannoside but not anti-alpha-linked mannoside antibodies produced after immunization with neoglycoproteins protect animals from disseminated candidiasis. In this study, peptides that mimic beta-1,2-linked mannosides were isolated using phage display methodology. A phage library expressing **random peptides** was panned with an anti-beta-1,2-linked mannoside monoclonal antibody (mAb). After three rounds of biopanning, the isolated phages were able to inhibit recognition of C. albicans by the mAb. Sixty percent of the phages had an identical DNA insert corresponding to the peptide sequence FHENWPS that was recognized specifically by the mAb. Injection of KLH-coupled peptide into mice generated high titers of polyclonal antibodies against C. albicans yeast cell walls. The anti-FHENWPS antibodies bound to C. albicans PPM and were inhibited by soluble beta-1,2-mannotetraose. Together, these data provide evidence for mimotopic activity of the peptide selected by biopanning with the anti-beta-1,2-oligomannoside mAb.

L10 ANSWER 11 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.

AB Random double-stranded oligonucleotides are useful reagents to identify the optimal binding sites for DNA-binding proteins, such as transcriptional activators. Some applications require ligation of random oligonucleotides to form plasmid-based libraries such as the yeast one-hybrid system, where the activation of a cloned DNA sequence from a library of random DNA-binding sequences activates a reporter gene. Current theories do not account for the low efficiencies of oligonucleotide-based plasmid library construction methods. We developed a technique to clone single oligonucleotides into plasmid vectors with high efficiency that predictably results in only one oligonucleotide insert per colony and used this method to clone a yeast one-hybrid library. This method, either as presented or with modifications, should be suitable for any situation where high-efficiency cloning of single oligonucleotide inserts is desired.

L10 ANSWER 12 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Activation domains (ADs) appear to work by making specific protein-protein contacts with the transcriptional machinery. However, ADs show no apparent sequence conservation, they can be functionally replaced by a number of **random peptides** and unrelated proteins, and their function does not depend on sustaining a complex tertiary structure. To gain a broader perspective on the nature of interactions between acidic ADs and several of their proposed targets, the in vivo strengths of viral, human, yeast, and artificial activation domains were determined under physiological conditions, and mutant ADs with increased in vivo potencies were selected. The affinities between ADs and proposed targets were determined in vitro and all interactions were found to be of low-level affinity with dissociation constants above 10-7 M. However, in vivo potencies of all ADs correlated nearly perfectly with their affinities for transcriptional proteins. Surprisingly, the weak interactions of the different ADs with at least two non-transcriptional proteins show the same rank order of binding and AD mutants selected for increased in vivo strength also have increased affinities to non-transcriptional proteins. Based on these results, isolated acidic ADs can bind with relatively low-level specificity and affinity to many different proteins and the strength of these semi-specific interactions determine the strength of an AD. I suggest that ADs expose flexible hydrophobic elements in an aqueous environment to contact hydrophobic patches over short distances, shifting specificity of activators largely to the DNA colocalization of arrays of ADs and targets.

L10 ANSWER 13 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Monoclonal antibody 6F5 (mAb 6F5), which recognizes the mycotoxin deoxynivalenol (DON) (vomitoxin), was used to select for peptides that mimic the mycotoxin by employing a library of filamentous phages that have **random** 7-mer **peptides** on their surfaces. Two phage clones selected from the random peptide phage-displayed library coded for the amino acid sequences SWGPFPF and SWGPLPF. These clones were designated DONPEP.2 and DONPEP.12, respectively. The results of a competitive enzyme-linked immunosorbent assay (ELISA) suggested that the two phage displayed peptides bound to mAb 6F5 specifically at the DON binding site. The amino acid sequence of DONPEP.2 plus a structurally flexible linker at the C terminus (SWGPF-PFGGGSC) was synthesized and tested to determine its ability to bind to mAb 6F5. This synthetic peptide (designated peptide C430) and DON competed with each other for mAb 6F5 binding. When translationally fused with bacterial alkaline phosphatase, DONPEP.2 bound specifically tomAb 6F5, while the fusion protein retained alkaline phosphatase activity. The potential of using DONPEP.2 as an immunochemical reagent in a DON immunoassay was evaluated with a DON-spiked wheat extract. When peptide C430 was conjugated to bovine serum albumin, it elicited antibody specific to peptide C430 but not to DON in both mice and rabbits. In an in vitro translation system containing rabbit reticulocyte lysate, synthetic peptide C430 did not inhibit protein synthesis but did show antagonism toward DON-induced protein synthesis inhibition. These data suggest that the peptides selected in this study bind to mAb 6F5 and

that peptide C430 binds to ribosomes at the same sites as DON.

L10 ANSWER 14 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB We describe a procedure for isolating agonists for mammalian G protein-coupled receptors of unknown function. Human formyl peptide receptor like-1 (FPRL-1) receptor, originally identified as an orphan G protein-coupled receptor related to the formyl peptide receptor (FPR1), was expressed in Saccharomyces cells designed to couple receptor activation to histidine prototrophy. Selection for histidine prototrophs among transformants obtained with a plasmid-based library encoding **random peptides** identified six different agonists, each of whose production yielded autocrine stimulation of the receptor expressed in yeast. A synthetic version of each peptide promoted activation of FPRL-1 expressed in human embryonic kidney (HEK293) cells, and five of the peptides exhibited significant selectivity for activation of FPRL-1 relative to FPR1. One selective peptide was tested and found to mobilize calcium in isolated human neutrophils. This demonstrates that stimulation of FPRL-1 results in neutrophil activation and suggests that the receptor functions as a component of the inflammatory response. This autocrin selection protocol may be a generally applicable method for providing pharmacological tools to evaluate the physiological roles of the growing number of mammalian orphan G protein-coupled receptors.

L10 ANSWER 15 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB We report the molecular mapping of the py-1 gene for resistance to corky root rot (Pyrenochaeta lycopersici (Schneider and Gerlach)) in tomato using RAPD and RFLP marker analysis. DNA from nearisogenic lines (NILs) of tomato differing in corky root rot resistance was screened with 575 **random oligonucleotide** primers to detect polymorphic DNAs linked to py-1. Three primers (OPW-04, OPC-02, OPG-19) revealed polymorphisms between the NILs. Twelve resistant and eight susceptible DNA pools derived from segregating F3 families were used to confirm that the RAPD markers were linked to the py-1 gene. Two of the linked amplified fragments, corresponding to OPW-04 and OPC-02, were subsequently cloned and mapped on the tomato molecular linkage map as RFLPs. These clones were located between TG40 and CT31 on the short arm of chromosome 3. Further analysis with selected RFLP markers showed that 7% (8.8 cM) of chromosome 3 of the resistant line 'Moboglan' was introgressed from the L. peruvianum donor parent. Three RFLP markers (TG40, TG324, and TG479) from the introgressed part of chromosome 3 were converted to cleaved amplified polymorphism (CAP) markers for use in a polymerase chain reaction (PCR) assay. These PCR markers will allow rapid large-scale screening of tomato populations for corky root rot resistance.

L10 ANSWER 16 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Genetic selections that use proteinaceous transdominant inhibitors encoded by DNA libraries to cause mutant phenocopies may facilitate genetic analysis in traditionally nongenetic organisms. We performed a selection for **random** short **peptides** and larger protein fragments (collectively termed "perturbagens") that inhibit the yeast pheromone response pathway. Peptide and protein fragment perturbagens that permit cell division in the presence of pheromone were recovered. Two perturbagens were derived from proteins required for pheromone response, and an additional two were derived from proteins that may negatively influence the pheromone response pathway. Furthermore, three known components of the pathway were identified as probable perturbagen targets based on physical interaction assays. Thus, by selection for transdominant inhibitors of pheromone response, multiple pathway components were identified either directly as gene fragments or indirectly as the likely targets of specific perturbagens. These results, combined with the results of previous work (Holzmayer, T. A., Pestov, D. G. & Roninson, I. B. (1992) Nucl. Acids. Res. 20, 711-717; Whiteway, M., Dignard, D. & Thomas, D. Y. (1992) Proc. Natl. Acad. Sci. USA 89, 9410-9414; and Gudkov, A. V., Kazarov, A. R., Thimmapaya, R., Axenovich, S. A., Mazo, 1. A. & Roninson, I. B. (1994) Proc. Natl. Acad. Sci. USA 91, 3744-3748), suggest that

transdominant genetic analysis of the type described here will be broadly applicable.

L10 ANSWER 17 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Four temperature isolates of Aspergillus fumigatus Fres. from Taiwan and six isolates from several culture collection centers (CBS, ATCC and IMI) were analyzed by **random** amplified polymorphic DNAs (RAPDs). Ten **oligonucleotide** decamers were used to generate selective markers from genomic DNAs and five primers gave adequate discrimination between isolates. All isolates were classified into four groups by RAPDs that consistent to their physiological characteristics. The results indicate that RAPDs analysis is useful to assess the genetic diversity and intraspecies temperature variation among different temperature strains of Aspergillus fumigatus.

L10 ANSWER 18 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB We have identified Xbp1 (XhoI site-binding protein 1) as a new DNA-binding protein with homology to the DNA-binding domain of the Saccharomyces cerevisiae cell cycle regulating transcription factors Swi4 and Mbp1. The DNA recognition sequence was determined by **random** **oligonucleotide** selection and confirmed by gel retardation and footprint analyses. The consensus binding site of Xbp1, GcCTCGA(G/A)G(C/A)g(a/g), is a palindromic sequence, with an XhoI restriction enzyme recognition site at its center. This Xbp1 binding site is similar to Swi4/Swi6 and Mbp1/Swi6 binding sites but shows a clear difference from these elements in one of the central core bases. There are binding sites for Xbp1 in the G-1 cyclin promoter (CLN1), but they are distinct from the Swi4/Swi6 binding sites in CLN1, and Xbp1 will not bind to Swi4/Swi6 or Mbp1/Swi6 binding sites. The XBP1 promoter contains several stress-regulated elements, and its expression is induced by heat shock, high osmolarity, oxidative stress, DNA damage, and glucose starvation. When fused to the LexA DNA-binding domain, Xbp1 acts as transcriptional repressor, defining it as the first repressor in the Swi4/Mbp1 family and the first potential negative regulator of transcription induced by stress. Overexpression of XBP1 results in a slow-growth phenotype, lengthening of G-1, an increase in cell volume, and a repression of G-1 cyclin expression. These observations suggest that Xbp1 may contribute to the repression of specific transcripts and cause a transient cell cycle delay under stress conditions.

L10 ANSWER 19 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Sixteen isolates of Cercospora sojina Hara, which causes the frog-eye leaf spot in soybean (Glycine max (L.) Merrill), collected in different regions of the state of Minas Gerais, Brazil, were characterized by RAPD analysis. Seventeen **random** **oligonucleotide** primers allowed for the amplification of 89 loci, 26 of them being polymorphic. Genetic distances among the isolates based on these data varied between 6 and 76%. Isolates collected in the same area were not necessarily clustered in the same group. The data demonstrate the extensive variability of C. sojina in the state of Minas Gerais, and opens up the possibility of a systematic classification of this pathogen by DNA-based molecular markers.

L10 ANSWER 20 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The DNA sequence of a fragment of 21731 bp (nucleotides 87408 to 109138) located on the left arm of chromosome VII from Saccharomyces cerevisiae S288C has been determined using a **random** cloning strategy followed by an **oligonucleotide**-directed sequencing. This fragment contains eight complete genes previously sequenced (CLG1, SK18, VAM7, YPT32, MIG2, SIP2, SPT16 and CHC1), the 5' part of POX1 and two other complete unidentified open reading frames of more than 100 amino acids.

L10 ANSWER 21 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB A library of **random** 10 residue **peptides** fused to the N-terminus of a reporter protein was screened in the yeast Saccharomyces

cerevisiae for sequences that can target the reporter for degradation by the N-end rule pathway a ubiquitin (Ub)-dependent proteolytic system that recognizes potential substrates through binding to their destabilizing N-terminal residues. One of the N-terminal sequences identified by this screen was used in a second screen for mutants incapable of degrading the corresponding reporter fusion. A mutant thus identified had an abnormally low content of free Ub. This mutant was found to be allelic to a previously isolated mutant in a Ub-dependent proteolytic system distinct from the N-end rule pathway. We isolated the gene involved, termed UFD3, which encodes an 80 kDa protein containing tandem repeats of a motif that is present in many eukaryotic proteins and called the WD repeat. Both co-immunoprecipitation and two hybrid assays demonstrated that Ufd3p is an in vivo ligand of Cdc48p, an essential ATPase required for the cell cycle progression and the fusion of endoplasmic reticulum membranes. Further, we showed that similarly to Ufd3p, Cdc48p is also required for the Ub-dependent proteolysis of test substrates. The discovery of the Ufd3p-Cdc48p complex and the finding that this complex is a part of the Ub system open up a new direction for studies of the function of Ub in the cell cycle and membrane dynamics.

L10 ANSWER 22 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB alpha-Factor, a 13-amino-acid pheromone secreted by haploid alpha cells of Saccharomyces cerevisiae, binds to Ste2p, a seven-transmembrane, G-protein-coupled receptor present on haploid a cells, to activate a signal transduction pathway required for conjugation and mating. To determine the structural requirements for alpha-factor activity, we developed a genetic screen to identify from **random** and semirandom libraries novel **peptides** that function as agonists or antagonists of Ste2p. The selection scheme was based on autocrine strains constructed to secrete **random peptides** and respond by growth to those that were either agonists or antagonists of Ste2p. Analysis of a number of peptides obtained by this selection procedure indicates that Trp1, Trp3, Pro8, and Gly9 are important for agonist activity specifically. His2, Leu4, Leu6, Pro10, a hydrophobic residue 12, and an aromatic residue 13 are important for both agonist and antagonist activity. Our results also show that activation of Ste2p can be achieved with novel, unanticipated combinations of amino acids. Finally, the results suggest the utility of this selection scheme for identifying novel ligands for mammalian G-protein-coupled receptors heterologously expressed in S. cerevisiae.

L10 ANSWER 23 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Thirty Italian isolates of the phytopathogenic fungus Ascochyta rabiei (Pass.) Labr., the causal organism of Ascochyta blight on chickpea (Cicer arietinum L.), were analysed by a **random oligonucleotide** primer dependent polymerase chain reaction (PCR) technique called random amplified polymorphic DNA analysis (RAPD) using three decamer primers. In previous investigations these isolates had been differentiated in six pathogenic groups. RAPD results were summarized in an analysis using the program PAUP. With each of the primers several amplification products were observed which were common to all isolates. The results of the RAPD analyses also showed that all isolates could be identified by a unique RAPD pattern. No correlation between RAPD patterns and the division of the isolates in pathogenic groups could be established. The application of the RAPD technique for cataloguing isolates and to obtain specific genetic markers for all isolates of the species Ascochyta rabiei is discussed.

L10 ANSWER 24 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Nineteen yeast colonies secreting rabies virus glycoprotein (G) peptides immunoreactive with polyclonal anti-rabies virus sera were selected from a **random** expression library. The **peptides**, around 80 amino acids long, spanned amino acids 54-494 of the G protein. These peptides, together with two constructions including, respectively, immunodominant sites II and III, were analysed for their immunoreactivity with 40 anti-G protein monoclonal antibodies (MAbs) composed of 12 MAbs that reacted with

SDS-treated protein in Western blot under reducing conditions (WB+) and 28 representative MAbs that did not react after denaturation (WB-). This last category represents 98 % of anti-rabies virus G MAbs. None of the WB- MAbs bound peptides. Of the 12 WB+ MAbs, one bound two peptides situated before the transmembrane domain of the protein and six bound peptides overlapping a region situated between amino acids 223 and 276. These six MAbs define a new antigenic region that would be considered 'immunodominant' if the peptide strategy had been used to study the antigenicity of the protein; however, this region is only recognized by about 1% of our MAbs. Three of these WB+ MAbs had significant neutralizing activity; two were used for the selection of antigenic mutants the region delimited by the peptides, confirming the (MAR mutants). Some mutants had a substitution within pertinence of both the peptide and escape mutant approaches. However, a few mutants had a substitution outside the peptide-delimited region, suggesting that remote mutations) could affect epitope accessibility in the native protein.

L10 ANSWER 25 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The application of random amplified polymorphic DNA (RAPD) analysis for the identification of ectomycorrhizal symbionts of spruce (Picea abies) belonging to the genera Boletus, Amanita and Lactarius at and below the species level was investigated. Using both fingerprinting (M13, (GTG)-5, (GACA)-4) as well as **random oligonucleotide** primers (V1 and V5), a high degree of variability of amplified DNA fragments (band-sharing index 65-80%) was detected between different strains of the same species, hence enabling the identification of individual strains within the same species. The band-sharing index between different species of the same genus (Boletus, Russula and Amanita) was in the range of 20-30%, and similar values were obtained when strains from different taxa were compared. Thus RAPD is too sensitive at this level of relationship and cannot be used to align an unknown symbiont to a given taxon. We therefore conclude that RAPD is a promising tool for the identification of individual strains, and could thus be used to distinguish indigenous and introduced mycorrhizal strains from the same species in natural ecosystems.

L10 ANSWER 26 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB A method to perform site-directed random mutagenesis directly in the yeast chromosomal DNA at the iso-1-cytochrome c-encoding gene locus (CYC1) is described. To test the effectiveness of the random mutagenesis procedure. the heme ligand His-18 was mutated to Ala (H18A), rendering cytochrome c (Cyc) nonfunctional. Random mutagenesis was performed by transforming yeast cells with a synthetic oligodeoxyribonucleotide (oligo) that randomizes the codon for His-18. The transformed cells were then selected for reversion to a functional Cyc on selective media. Ten functional mutants were recovered, all of which had integrated the synthetic oligo. Sequencing showed that five of the recovered mutants carried the His codon, CAU, and five mutants contained the His codon, CAC. Because Arg had previously been found as a heme ligand, this mutant was produced by standard techniques and integrated into the yeast chromosome. These yeast did not produce a holo cytochrome c that was detectable by low-temperature spectroscopy. To develop a selection for nonfunctional Cyc, competent yeast (which tack the ability to synthesize tryptophan) were cotransformed with a plasmid carrying the TRP1 gene and the **random oligo**, and were plated on media tacking tryptophan. Of the 1200 colonies that grew, 120 tested negative for the integration of the **random oligo**, demonstrating that this particular selection for nonfunctional protein is not feasible. A method is thus described for directed, random mutagenesis directly in the yeast chromosome that can be used to probe structure/function relationships in Cyc. Only His can act as a heme ligand at position 18, using the functional selection described here.

L10 ANSWER 27 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB We report the DNA sequence of a segment located on the right arm of

chromosome II from Saccharomyces cerevisiae S288C near the subtelomeric sequences. The sequence was determined using a **random** cloning strategy followed by an **oligonucleotide**-directed sequencing. The segment contains four non-overlapping open reading frames (ORFs) YBR297w, YBR298c, YBR299w and YBR301c, and two overlapping ones (YBR300c and YBR300w). Three of them-YBR297w, YBR298c and YBR299w-are the MAL3R (transcriptional regulatory protein), MAL3T (maltose permease) and MAL3S (maltase) genes of the MAL3 locus previously localized. The three other ORFs are unidentified. Another MAL locus (MAL1) has been localized on chromosome VII. The Mal-phenotype of strain S288c cannot be explained by telomeric silencing. The sequences have been submitted to the EMBL data library under Accession Numbers Z36166; Z36167; Z36168; Z36169 and Z36171.

L10 ANSWER 28 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The yeast two-hybrid system was used to screen a library of **random peptides** fused to a transcriptional activation domain in order to identify peptides capable of binding to the retinoblastoma protein (Rb). Seven peptides were identified, all of which contain the Leu-X-Cys-X-Glu motif found in Rb-binding proteins, although their activity in the yeast assay varied over a 40-fold range. Mutagenesis of the DNA encoding two of these peptides followed by screening in the two-hybrid system allowed the delineation of residues apart from the invariant Leu, Cys and Glu that affect binding to Rb. Binding affinities of a peptide and one of its variants to Rb, determined by surface plasmon resonance, correlated with results from the two-hybrid assay. This method offers several advantageous features compared to existing technology for screening peptide libraries: in vivo detection of protein-peptide interactions, high sensitivity, the capacity for rapid genetic screening to identify stronger and weaker binding peptide variants, and the use of a simple assay (transcriptional activity) as a means to assess binding affinity.

L10 ANSWER 29 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Didymella bryoniae (anamorph Phoma cucurbitacearum), which causes gummy stem blight of cucurbits, occurs throughout the eastern United States. Other Phoma spp., such as P. exigua, also have been reported to cause symptoms of gummy stem blight. Twenty-seven isolates provisionally identified as D. bryoniae or Phoma spp. were obtained from diseased watermelon, cantaloupe, cucumber, pumpkin, and squash grown in South Carolina, New York, and Florida. D. bryoniae was clearly distinguished from Phoma after 7 days of growth on quarter-strength potato-dextrose agar at 24 C with a 12-h photoperiod. D. bryoniae produced white aerial mycelium, olivaceous green substrate mycelium, and few pycnidia; Phoma produced sparse aerial mycelium and numerous pycnidia, sometimes in concentric zones. The percent monoseptate conidia for D. bryoniae isolates ranged from 0 to 18%, whereas no Phoma isolate produced any septate conidia. Seventeen of 19 D. bryoniae isolates were pathogenic on watermelon cv. Charleston Gray and cantaloupe cv. Classic; all eight isolates of Phoma and two isolates of D. bryoniae were nonpathogenic. Genomic DNA was extracted from all 27 isolates described above plus two additional isolates of D. bryoniae from New York and one from Florida. DNA was amplified using PCR primed with **random oligonucleotide** decamers. RAPD amplification patterns clearly differentiated D. bryoniae from Phoma. Each of five primers used produced two to four amplified fragments that were unique either to all D. bryoniae or to all Phoma isolates. Thirteen additional fragments were present in all D. bryoniae isolates except two of the three isolates from New York.

L10 ANSWER 30 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The genetic structure of Pyrenophora teres, an ascomycete fungus that causes net blotch of barley, was examined using random amplified polymorphic DNA (RAPD) markers. Twenty-seven **random oligonucleotide** primers were screened against DNA from 16 isolates of P. teres of diverse geographic origin. Five primers gave scorable, reproducible DNA products (bands) suitable for population genetic studies. Genetic analyses of bands produced by two of the primers revealed single

locus segregation in three of four crosses, indicating that these RAPDs can be interpreted as alleles at genetic loci. Allele frequencies were determined for 10 putative RAPD loci from five primers in 22-35 isolates of P. teres sampled from each of five geographically separated populations in Canada, Germany, and the U.S.A. Eight RAPD loci were polymorphic in at least one population and two loci were monomorphic in all five populations. Variation in allele frequencies (allelic diversity) among the five populations was partitioned into within- and among-population components using Nei's G-ST. A G-ST value of 0.46 was obtained among all populations indicating that approximately 46% of the total genetic variability detected was due to differentiation among populations compared with 54% within populations. A G-ST value of 0.33 was obtained among the North American populations only. From five to nine multilocus genotypes were found in each population. Nine genotypes occurred exclusively in the German population and four exclusively in the New York population. The other populations had one or two unique genotypes. Gametic disequilibrium values (nonrandom associations of RAPD loci) were calculated among all pairs of polymorphic loci within each population. Eleven of 49 values were significantly different from 0 (P lt 0.05); 8 of the 11 significant gametic disequilibrium values occurred in the New York population. Highly significant gametic disequilibrium was detected between the same two RAPD loci in three different populations, suggesting that these loci are genetically linked. Two different multilocus analyses revealed that the genetic structures of the Alberta, North Dakota, and German populations but not the New York population were consistent with random sexual reproduction occurring in these populations.

L10 ANSWER 31 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB A powerful and versatile system for the identification of novel response elements for members of the intracellular receptor family is presented as applied to the human estrogen receptor. In the past, a limited number of estrogen response elements (EREs) have been functionally identified in the promoter regions of estrogen-regulated genes. From these a consensus ERE has been defined that is identical to the ERE of the Xenopus laevis vitellogenin gene, i.e., 5'GGTCA NNN TGACC-3'. In order to investigate without bias the range of sequences that could function as EREs In vivo, we have developed a genetic selection in yeast expressing the human estrogen receptor (hER) and transformed with a **random oligonucleotide** library in a vector where expression of a selectable marker requires insertion of an upstream activating sequence. More than 1,000,000 transformants were screened and of 726 clones that contained activating sequences, 65 were found to be hormone-dependent. Sequencing revealed that the majority contained at least one 4/5 match to a canonical ERE half-site, but only one contained a full consensus ERE as previously defined. Some contained half-sites arranged as direct repeats. Twelve elements were further characterized to compare estrogen activation in yeast and mammalian cells and In vitro binding to hER. The results of these studies reveal that sequences that bind weakly to hER in vitro are fully functional as EREs in yeast and are conditionally responsive to estrogen in mammalian cells. In addition, an element was identified that is more sensitive to the partial agonist activities of tamoxifen and nafoxidine than is the consensus ERE, indicating that not only promoter context but the sequence of the binding site itself can allow distinction between receptor activated by agonist and that activated by antagonist.

L10 ANSWER 32 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB The a-factor of Saccharomyces cerevisiae (YIIKGVFWDPAC(Farnesyl)-OCH-3) is a peptide pheromone in which post-translational modification with a farnesyl isoprenoid and carboxyl methyl group s required for export and bioactivity. Truncated and carboxyl-terminal modified analogs of the a-factor were synthesized in order to determine the effect of such modifications on bioactivity. Bioactivity studies on carboxyl-terminal analogs in which the chirality, the cysteine thioether, and the carboxyl ester were varied in an attempt to study the influence of topology on a-factor activity indicate that the hydrophobicity conferred by the

farnesyl moiety and not its specific spatial orientation is a key determinant of a-factor potency. Analyses on truncated a-factors suggest that sequential removal of NH-2-terminal residues leads to a gradient of potency loss, with some amino acids exhibiting a slightly greater contribution to bioactivity than others. **Random oligonucleotide**-targeted mutagenesis of the gene encoding a-factor was coupled to a biological screen to identify altered a-factor peptides which are secreted yet exhibit a loss of a-factor bioactivity. Transformants exhibiting this phenotype were examined to identify codon changes presumably responsible for the altered phenotype, thus indicating residues that may contribute significantly to a-factor bioactivity.

L10 ANSWER 33 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB A set of 420 **random**, 10-base. **oligonucleotide** primers was screened for random amplified polymorphic DNA (RAPD) fragments within a sample of eight megagametophyte DNAs of a single slash pine (Pinus elliottii Engelm. var. elliottii) tree. The apparently repeatable RAPD fragments were further characterized within a sample of 68 megagametophytes from the same tree. Fragments segregating in a 1:1, present-to-absent, ratio were classified and mapped using multi-point linkage analysis. The analysis revealed 13 linkage groups of at least three loci. ranging in size from 28 to 68 cM, and nine linked pairs of loci. The 22 groups and pairs included 73 RAPD markers and covered a genetic map distance of approximately 782 cM. Genome size estimates, based on linkage data, ranged from 2880 to 3360 cM. Using a 30-cM map scale and including the 24 unlinked markers and the ends of the 13 linkage groups and nine linked pairs, the set of RAPD markers accounts for approximately 2160 cM or 64-75% of the genome. This extent of genomic coverage should allow for the efficient mapping, of genes responsible for a reaction to the causal agent of fusiform rust disease, Cronartium quercuum (Berk.) Miyabe ex Shirai f. sp. fusiforme.

L10 ANSWER 34 OF 34 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
AB Carboxypeptidase Y from yeast contains a free sulfhydryl group (Cys341) which is important to the catalytic efficiency and the stability of the enzyme. A number of mutant enzymes have been constructed using a semi-**random oligonucleotide** directed mutagenesis method. Mutant enzyme, in which Cys341 had been replaced by Ser, Gly, Gln and Glu, were subjected to kinetic analysis and found to have greatly reduced activities towards a wide range of dipeptide and ester substrates. However, for the Glu341 substituted enzyme the activity towards Bz-Lys-OMe was 4 fold higher than that of the wild type enzyme. The thermal stability as well as pH stabilities of these mutated enzymes were significantly reduced as compared with wild type carboxypeptidase Y, and the enzymes containing His and Lys at position 341 were inactive. The possible functional relation between Cys341 of carboxypeptidase Y and the free cysteinyl group (Cys72) of proteinase K from Tritirachium album Limber is discussed.

=> log y

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|---|---|---|
| FULL ESTIMATED COST | 151.27 | 195.00 |

| DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS) | SINCE FILE ENTRY | TOTAL SESSION |
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